

43072-0002PC.TXT

SEQUENCE LISTING

<110> ExSAR Corporation
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<120> Drug Candidate Selection by Hydrogen
Exchange Characterization of Ligand-Induced Receptor
Conformation

<130> 43072-0002 PC

<160> 2

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 266

<212> PRT

<213> Artificial Sequence

<220>

<223> Homo sapiens PPAR gamma ligand binding domain

<400> 1

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Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro
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Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp
 20     25     30
Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu
 35     40     45
Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys
 50     55     60
Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu
 65     70     75     80
Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val
 85     90     95
Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His
100     105    110
Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val
115     120    125
Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser
130     135    140
Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala
145     150    155    160
Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe
165     170    175
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val
180     185    190
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu
195     200    205
Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu
210     215    220
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln
225     230    235    240
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro
245     250    255
Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
260     265

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<210> 2

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<400> 2

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Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
1      5      10      15
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
20
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
35      40      45
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
50      55      60
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
65      70      75      80
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
85      90      95
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
100      105      110
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
115      120      125
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
130      135      140
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
145      150      155      160
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
165      170      175
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
180      185      190
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
195      200      205
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
210      215      220
Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
225      230      235      240
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
245      250      255
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
260      265      270
Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
275      280      285
Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
290      295      300
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
305      310      315      320
Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
325      330      335
Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
340      345      350
Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
355      360      365
Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
370      375      380
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
385      390      395      400
Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
405      410      415
Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
420      425      430
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
435      440      445
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
450      455      460
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
465      470      475      480
Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
485      490      495
Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
500      505

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